

PCTWORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁷ : C07K 14/37, C12Q 1/68, G06F 17/30, 19/00	A2	(11) International Publication Number: WO 00/56762 (43) International Publication Date: 28 September 2000 (28.09.00)
(21) International Application Number: PCT/US00/07781 (22) International Filing Date: 22 March 2000 (22.03.00) (30) Priority Data: 09/273,623 22 March 1999 (22.03.99) US (71) Applicants: NOVO NORDISK BIOTECH, INC. [US/US]; 1445 Drew Avenue, Davis, CA 95616 (US). NOVO NORDISK A/S [DK/DK]; Novo Alle, DK-2880 Bagsvaerd (DK). (72) Inventors: BERKA, Randy, M.; 3609 Modoc, Davis, CA 95616 (US). REY, Michael, W.; 605 Robin Place, Davis, CA 95616 (US). SHUSTER, Jeffrey, R.; 2619 Regatta Lane, Davis, CA 95616 (US). KAUPPINEN, Sakari; Norskekrogen 12, DK-2765 Smørum (DK). CLAUSEN, Ib, Groth; Fyrrestien 6, DK-3400 Hillerød (DK). OLSEN, Peter, Bjarke; Svendborggade 8, 4tv, DK-2100 Copenhagen (DK). (74) Agents: ZELSON, Steve, T. et al.; Novo Nordisk of North America, Inc., 405 Lexington Avenue, Suite 6400, New York, NY 10174 (US).		(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>Without international search report and to be republished upon receipt of that report.</i>
(54) Title: METHODS FOR MONITORING MULTIPLE GENE EXPRESSION (57) Abstract The present invention relates to methods for monitoring differential expression of a plurality of genes in a first filamentous fungal cell relative to expression of the same genes in one or more second filamentous fungal cells using microarrays containing filamentous fungal expressed sequenced tags. The present invention also relates to filamentous fungal expressed sequenced tags and to computer readable media and substrates containing such expressed sequenced tags for monitoring expression of a plurality of genes in filamentous fungal cells.		

Table 4. *Trichoderma reesei* ESTs

Sequence Listing	zscore	Annotation	Database	Functional Category
7401	3514.6	EXOGLUCANASE I PRECURSOR (EC 3.2.1.91) (EXOCELLOBIOHYDROLASE I) (CBHI) (1,4-BETA-CELLOBIOHYDROLASE).	swissprot P00725	ND
7402	3143.2	Cellobiohydrolase CBH II protein.	geneseqp P50308	ND
7403	2899.7	HEAT SHOCK 70 KD PROTEIN (HSP70).	swissprot Q01233	Posttranslational modification, protein turnover, chaperones
7404	2335.7	BETE-GLUCOSIDASE.	sptrembl O93785	ND
7405	2276.9	BETA-XYLOSIDASE PRECURSOR (EC 3.2.1.37).	sptrembl Q92458	ND
7406	2270.7	PROTEIN DISULPHIDE ISOMERASE PRECURSOR.	sptrembl O74568	ND
7407	1899.1	ENDOGLUCANASE IV.	sptrembl O14405	ND
7408	1808.4	ENDOGLUCANASE EG-II PRECURSOR (EC 3.2.1.4) (ENDO-1,4-BETA-GLUCANASE) (CELLULASE).	swissprot P07982	ND
7409	1731.4	Enzyme with endoglucanase activity.	geneseqp R66548	ND
7410	1719.7	Endoglucanase-I protein sequence.	geneseqp R79539	ND
7411	1691.7	ACETYLXYLAN ESTERASE PRECURSOR (EC 3.1.1.72).	sptrembl Q99034	ND
7412	1640.1	PUTATIVE PROTEASE SUBUNIT, CHAPERONIN.	sptrembl O94641	Posttranslational modification, protein turnover, chaperones
7413	1526.2	ELONGATION FACTOR I-ALPHA (EF-1-ALPHA).	swissprot P34825	Amino acid transport and metabolism
7414	1453.5	78 KD GLUCOSE-REGULATED PROTEIN HOMOLOG PRECURSOR (GRP 78) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG) (BIP).	swissnew P78695	Posttranslational modification, protein turnover, chaperones
7415	1408.0	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE 2 (EC 1.2.1.12) (GAPDH2).	swissprot P17730	Carbohydrate transport and metabolism
7416	1405.7	AMINO-ACID PERMEASE IND1.	swissprot P34054	Amino acid transport and metabolism
7417	1395.0	NADH DEHYDROGENASE SUBUNIT.	sptrembl Q01388	Energy production and conversion
7418	1393.9	POLYUBIQUITIN.	sptrembl O74274	ND

Table 4. *Trichoderma reesei* ESTs

Sequence Listing	zscore	Annotation	Database	Functional Category
7401	3514.6	EXOGLUCANASE I PRECURSOR (EC 3.2.1.91) (EXOCELLOBIOHYDROLASE I) (CBHI) (1,4-BETA-CELLOBIOHYDROLASE).	swissprot P00725	ND
7402	3143.2	Cellobiohydrolase CBH II protein.	geneseqp P50308	ND
7403	2899.7	HEAT SHOCK 70 KD PROTEIN (HSP70).	swissprot Q01233	Posttranslational modification, protein turnover, chaperones
7404	2335.7	BETE-GLUCOSIDASE.	sptrembl O93785	ND
7405	2276.9	BETA-XYLOSIDASE PRECURSOR (EC 3.2.1.37).	sptrembl Q92458	ND
7406	2270.7	PROTEIN DISULPHIDE ISOMERASE PRECURSOR.	sptrembl O74568	ND
7407	1899.1	ENDOGLUCANASE IV.	sptrembl O14405	ND
7408	1808.4	ENDOGLUCANASE EG-II PRECURSOR (EC 3.2.1.4) (ENDO-1,4-BETA-GLUCANASE) (CELLULASE).	swissprot P07982	ND
7409	1731.4	Enzyme with endoglucanase activity.	geneseqp R66548	ND
7410	1719.7	Endoglucanase-I protein sequence.	geneseqp R79539	ND
7411	1691.7	ACETYLXYLAN ESTERASE PRECURSOR (EC 3.1.1.72).	sptrembl Q99034	ND
7412	1640.1	PUTATIVE PROTEASE SUBUNIT, CHAPERONIN.	sptrembl O94641	Posttranslational modification, protein turnover, chaperones
7413	1526.2	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA).	swissprot P34825	Amino acid transport and metabolism
7414	1453.5	78 KD GLUCOSE-REGULATED PROTEIN HOMOLOG PRECURSOR (GRP 78) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG) (BIP).	swissnew P78695	Posttranslational modification, protein turnover, chaperones
7415	1408.0	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE 2 (EC 1.2.1.12) (GAPDH2).	swissprot P17730	Carbohydrate transport and metabolism
7416	1405.7	AMINO-ACID PERMEASE INDA1.	swissprot P34054	Amino acid transport and metabolism
7417	1395.0	NADH DEHYDROGENASE SUBUNIT.	sptrembl Q01388	Energy production and conversion
7418	1393.9	POLYUBIQUITIN.	sptrembl O74274	ND

7419	1346.1	ADP,ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE TRANSLOCATOR) (ANT).	swissprot P02723	ND
7420	1323.7	PYRUVATE CARBOXYLASE.	sptrembl O93918	Amino acid transport and metabolism
7421	1309.3	GLUCAN SYNTHASE.	sptrembl Q9Y8B3	ND
7422	1262.0	BETA-XYLOSIDASE PRECURSOR (EC 3.2.1.37).	sptrembl Q92458	ND
7423	1257.6	HEAT SHOCK PROTEIN 90 HOMOLOG (SUPPRESSOR OF VEGETATIVE INCOMPATIBILITY MOD-E).	swissprot O43109	Posttranslational modification, protein turnover, chaperones
7424	1236.9	ALPHA-L-ARABINOFURANOSIDASE PRECURSOR (EC 3.2.1.55) (ARABINOSIDASE).	swissprot O54161	ND
7425	1236.1	STRESS-RESPONSIVE GENE PRODUCT.	tremblnew BAA85305	ND
7426	1233.4	T. longibrachiatum endoglucanase EGII.	geneseqp R77264	ND
7427	1209.2	EXOGLUCANASE I PRECURSOR (EC 3.2.1.91) (EXOCELLIOHYDROLASE I) (CBHI) (1,4-BETA-CELLOBIOHYDROLASE).	swissprot P00725	ND
7428	1202.4	ACID TREHALASE PRECURSOR (EC 3.2.1.28) (ALPHA,ALPHA-TREHALASE) (ALPHA,ALPHA-TREHALOSE GLUCOHYDROLASE).	swissprot P78617	ND
7429	1180.9	A. chrysogenum gamma-actin.	geneseqp W77101	Cell division and chromosome partitioning
7430	1175.1	SERINE HYDROXYMETHYLTRANSFERASE, CYTOSOLIC (EC 2.1.2.1) (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT).	swissprot P34898	Amino acid transport and metabolism
7431	1158.1	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA).	swissprot P34825	Amino acid transport and metabolism
7432	1155.9	RIBOSE-PHOSPHATE PYROPHOSPHOKINASE.	sptrembl O94413	Nucleotide transport
7433	1140.3	NAD(+)-ISOCITRATE DEHYDROGENASE SUBUNIT I PRECURSOR.	sptrembl O13302	Amino acid transport and metabolism
7434	1132.8	PLASMA MEMBRANE ATPASE (EC 3.6.1.35) (PROTON PUMP).	swissprot P07038	Inorganic ion transport and metabolism
7435	1127.0	HISTIDINE KINASE (FRAGMENT).	tremblnew AAD40816	ND
7436	1122.6	HYPOTHETICAL 44.2 KD GTP-BINDING PROTEIN IN SCO2-MRF1 INTERGENIC REGION.	swissprot P38219	ND

7437	1073.9	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (CROSS-PATHWAY CONTROL WD-REPEAT PROTEIN CPC-2).	swissprot Q01369	ND
7438	1063.3	GTP-BINDING PROTEIN YPT1.	swissprot P33723	ND
7440	993.7	FUMARATE HYDRATASE PRECURSOR (EC 4.2.1.2) (FUMARASE).	swissprot P55250	Energy production and conversion
7441	985.3	PH RESPONSIVE PROTEIN 1 PRECURSOR (PH-REGULATED PROTEIN 1).	swissprot P43076	ND
7442	985.0	60S RIBOSOMAL PROTEIN L5.	swissprot O59953	Translation, ribosomal structure and biogenesis
7443	980.7	INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE).	swissprot P19117	Energy production and conversion
7444	977.7	40S RIBOSOMAL PROTEIN S3AE (S1).	swissprot P40910	Translation, ribosomal structure and biogenesis
7445	971.3	MONOUBIQUITIN/CARBOXY EXTENSION PROTEIN FUSION.	sptrembl O74216	ND
7446	968.6	PROBABLE ATP-DEPENDENT PERMEASE C3F10.11C.	swissprot Q10185	ND
7447	959.7	HEAT SHOCK PROTEIN 90 HOMOLOG (SUPPRESSOR OF VEGETATIVE INCOMPATIBILITY MOD-E).	swissprot O43109	Posttranslational modification, protein turnover, chaperones
7448	957.2	CYCLOPHILIN B (EC 5.2.1.8).	sptrembl O94190	Posttranslational modification, protein turnover, chaperones
7450	944.8	AMINO-ACID PERMEASE IND1.	swissprot P34054	Amino acid transport and metabolism
7451	936.4	PLASMA MEMBRANE H(+)-ATPASE.	sptrembl O93862	Inorganic ion transport and metabolism
7452	925.1	78 KD GLUCOSE-REGULATED PROTEIN HOMOLOG PRECURSOR (GRP 78) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG) (BIP).	swissnew P78695	Posttranslational modification, protein turnover, chaperones
7453	907.3	PUTATIVE BETA-SUBUNIT OF K ⁺ CHANNELS.	sptrembl O82064	Energy production and conversion
7454	902.5	CHROMOSOME XV READING FRAME ORF YOR262W.	sptrembl Q08726	ND
7455	900.3	ACYL-COA DESATURASE 1 (EC 1.14.99.5) (STEAROYL-COA DESATURASE 1) (FATTY ACID DESATURASE 1).	sptrembl Q12618	Lipid metabolism

7456	899.4	PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.	swissprot P78979	Cell motility and secretion
7457	876.0	60S RIBOSOMAL PROTEIN L23 (L17).	swissprot P04451	Translation, ribosomal structure and biogenesis
7458	867.5	BETA-GLUCOSIDASE.	sptrembl O93784	ND
7459	861.2	78 KD GLUCOSE-REGULATED PROTEIN HOMOLOG PRECURSOR (GRP 78) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG) (BIP).	swissnew P78695	Posttranslational modification, protein turnover, chaperones
7460	856.5	PUTATIVE GTP CYCLOHYDROLASE.	tremblnew CAB65619	ND
7461	849.6	PROTEASOME COMPONENT PUP2 (EC 3.4.99.46) (MACROPAIN SUBUNIT PUP2) (PROTEINASE YSCE SUBUNIT PUP2) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT PUP2).	swissprot P32379	Posttranslational modification, protein turnover, chaperones
7462	839.0	40S RIBOSOMAL PROTEIN S4.	swissprot P87158	Translation, ribosomal structure and biogenesis
7463	837.8	PCZA361.14.	sptrembl O52801	ND
7464	835.2	CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).	swissprot P87072	ND
7465	834.2	3-ISOPROPYLMALATE DEHYDROGENASE (EC 1.1.1.85) (BETA-IPM DEHYDROGENASE) (IMDH) (3-IPM-DH).	swissprot P34738	Amino acid transport and metabolism
7466	832.8	HEAT SHOCK PROTEIN 60 PRECURSOR (ANTIGEN HIS-62).	swissprot P50142	Posttranslational modification, protein turnover, chaperones
7467	829.9	40S RIBOSOMAL PROTEIN S17 (CRP3).	swissprot P27770	Translation, ribosomal structure and biogenesis
7468	823.2	4-DIHYDROMETHYL-TRISPORATE DEHYDROGENASE.	sptrembl Q01213	ND
7469	801.8	CYCLOPHILIN, MITOCHONDRIAL FORM PRECURSOR (EC 5.2.1.8).	sptrembl Q99009	Posttranslational modification, protein turnover, chaperones
7470	800.4	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (EC 3.6.1.34).	swissnew P23704	Energy production and conversion
7471	797.6	A. niger xylanase regulator xylR.	geneseqp W08586	ND

7472	796.4	40S RIBOSOMAL PROTEIN S8 (S14) (YS9) (RP19).	swissprot P05754	Translation, ribosomal structure and biogenesis
7473	787.3	60S RIBOSOMAL PROTEIN L2.	sptrembl O94253	Translation, ribosomal structure and biogenesis
7474	780.1	ELONGATION FACTOR 2 (FRAGMENT).	tremblnew CAB52147	Translation, ribosomal structure and biogenesis
7475	778.8	VACUOLAR ATP SYNTHASE SUBUNIT B (EC 3.6.1.34) (V-ATPASE 57 KD SUBUNIT).	swissprot P11593	Energy production and conversion
7476	778.0	40S RIBOSOMAL PROTEIN S14 (CRP2).	swissprot P19115	Translation, ribosomal structure and biogenesis
7477	757.6	PROBABLE UTP--GLUCOSE-1-PHOSPHATE URIDYLTRANSFERASE.	tremblnew CAA22857	ND
7478	746.3	Candida albicans CaCLA4 protein.	geneseqp W48896	Signal transduction mechanisms
7479	736.5	CTR1 SUPPRESSOR PROTEIN.	swissprot P32784	ND
7480	728.0	ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL-ACTIVATING ENZYME).	swissprot P16928	Lipid metabolism
7481	725.0	TRANSALDOLASE (EC 2.2.1.2).	swissprot P15019	Carbohydrate transport and metabolism
7482	724.0	PROTEIN KINASE.	sptrembl O59790	Signal transduction mechanisms
7483	720.8	PDI RELATED PROTEIN A.	sptrembl O93914	Energy production and conversion
7484	711.9	40S RIBOSOMAL PROTEIN S22 (S15A) (YS24).	swissprot P33953	Translation, ribosomal structure and biogenesis
7485	709.2	Yeast RNA-binding protein ZPR1.	geneseqp W38455	ND
7486	700.7	pI 5.5 endoxylanase.	geneseqp R47123	ND
7487	700.5	PUTATIVE ALPHA,ALPHA-TREHALOSE-PHOSPHATE SYNTHASE.	tremblnew CAB52715	Carbohydrate transport and metabolism
7488	693.1	POTENTIAL PROTEASOME COMPONENT C5 (EC 3.4.99.46) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C5).	swissprot P23724	Posttranslational modification, protein turnover, chaperones

7489	684.0	VACUOLAR ASPARTIC PROTEASE PRECURSOR.	sptrembl O42630	ND
7490	682.5	PHOSPHOGLUCOMUTASE.	sptrembl O74374	Carbohydrate transport and metabolism
7491	681.8	40S RIBOSOMAL PROTEIN S6.	swissprot P05752	Translation, ribosomal structure and biogenesis
7492	678.4	PROTEIN TRANSPORT PROTEIN SEC13.	swissprot P53024	ND
7493	667.9	EBURICOL 14 ALPHA-DEMETHYLASE.	tremblnew AAF18468	ND
7494	663.8	NADP-SPECIFIC GLUTAMATE DEHYDROGENASE (EC 1.4.1.4) (NADP-GDH).	swissprot P00369	Amino acid transport and metabolism
7495	653.0	HYPOTHETICAL 17.4 KD PROTEIN.	sptrembl O59727	ND
7496	643.2	DIHYDROLIPOAMIDE ACETYLTRANSFERASE COMPONENT OF PYRUVATE DEHYDROGENASE COMPLEX, MITOCHONDRIAL PRECURSOR (EC 2.3.1.12) (E2) (PDC-E2) (MRP3).	swissprot P20285	Energy production and conversion
7497	641.3	CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT.	sptrembl Q9Y777	Signal transduction mechanisms
7498	639.5	CELL DIVISION-ASSOCIATED PROTEIN BIMB.	swissprot P33144	ND
7499	632.0	HIGH-AFFINITY GLUCOSE TRANSPORTER.	swissprot P49374	ND
7500	631.2	HYPOTHETICAL 58.8 KD PROTEIN C16A3.10 IN CHROMOSOME II.	sptrembl O42916	ND
7501	628.2	PROTEIN KINASE DSK1 (EC 2.7.1.-) (DIS1-SUPPRESSING PROTEIN KINASE).	swissprot P36616	Signal transduction mechanisms
7502	627.2	14-3-3.	tremblnew BAA89421	ND
7503	623.1	78 KD GLUCOSE-REGULATED PROTEIN HOMOLOG PRECURSOR (GRP 78) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG) (BIP).	swissprot P36604	Posttranslational modification, protein turnover, chaperones
7504	618.5	CYTOCHROME C549.	tremblnew BAA85768	ND
7505	617.0	3-HYDROXYBUTYRYL-COA DEHYDROGENASE (EC 1.1.1.157) (BETA- HYDROXYBUTYRYL-COA DEHYDROGENASE) (BHBD).	swissprot Q45223	Lipid metabolism
7506	616.9	HEAT SHOCK 70 KD PROTEIN COGNATE 5.	swissprot P29845	Posttranslational modification, protein turnover, chaperones
7507	607.2	01232.	sptrembl Q05663	ND

7508	605.9	SERINE THREONINE-PROTEIN KINASE.	sptrembl O94537	Signal transduction mechanisms
7509	597.9	FRUCTOSE-1,6-BISPHOSPHATASE (EC 3.1.3.11) (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE).	swissprot P09202	Carbohydrate transport and metabolism
7510	593.3	NADH-DEPENDENT GLUTAMATE SYNTHASE.	sptrembl Q40360	Amino acid transport and metabolism
7511	585.6	AVICELASE III.	sptrembl O74170	ND
7512	577.5	HISTONE H4.1.	swissprot P23750	DNA replication, recombination and repair
7513	572.1	GLYCEROL-3-PHOSPHATE DEHYDROGENASE (FRAGMENT).	tremblnew AAB50200	Energy production and conversion
7514	568.8	HEAT SHOCK PROTEIN HSP88.	sptrembl O74225	ND
7515	564.0	DOLICHOL-PHOSPHATE MANNOSYLTRANSFERASE (EC 2.4.1.83) (DOLICHOL-PHOSPHATE MANNOSE SYNTHASE) (DOLICHYL-PHOSPHATE BETA-D-MANNOSYLTRANSFERASE).	sptrembl O14466	ND
7516	552.8	PROBABLE SYNAPTOBREVIN HOMOLOG C6G9.11.	swissprot Q92356	ND
7517	552.8	60S RIBOSOMAL PROTEIN L1-B (L10A).	swissprot O74836	Translation, ribosomal structure and biogenesis
7518	551.9	VANILLIN: NAD+ OXIDOREDUCTASE.	sptrembl O69763	ND
7519	545.5	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE (EC 4.2.1.-); D-3-HYDROXYACYL COA DEHYDROGENASE (EC 1.1.1.-)].	swissnew Q01373	ND
7520	543.1	UREASE (EC 3.5.1.5) (UREA AMIDOHYDROLASE).	sptrembl O14420	Amino acid transport and metabolism
7521	541.4	PUTATIVE SECRETED HYDROLASE.	sptrembl O69962	ND
7522	540.4	60S RIBOSOMAL PROTEIN L13.	swissprot O59931	ND
7523	535.2	BETA-GLUCOSIDASE PRECURSOR (EC 3.2.1.21) (GENTIOBIASE) (CELLOBIASE) (BETA-D-GLUCOSIDE GLUCOHYDROLASE).	swissprot <u>P07337</u>	ND
7524	532.0	PUTATIVE TRANSCRIPTIONAL REPRESSOR C30D10.02.	sptrembl O14348	ND
7525	523.6	MYOSIN I HEAVY CHAIN.	sptrembl Q00647	ND

7526	521.8	PUTATIVE MITOCHONDRIAL CARRIER C8C9.12C.	sptrembl O14281	ND
7527	520.3	MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR (EC 1.1.1.37).	swissprot P17505	Energy production and conversion
7528	518.6	U6 SNRNA-ASSOCIATED SM-LIKE PROTEIN LSM5.	tremblnew AAD56229	ND
7529	511.2	PHOSPHOGLUCOMUTASE I (EC 5.4.2.2) (GLUCOSE PHOSPHOMUTASE I) (PGM I).	swissprot P33401	Carbohydrate transport and metabolism
7530	510.1	Yeast CAAX processing enzyme Afc1p.	geneseqp W48301	Posttranslational modification, protein turnover, chaperones
7531	507.9	c424 gene product.	geneseqp R43654	ND
7532	505.8	PURINE NUCLEOSIDE PERMEASE.	sptrembl O93844	ND
7533	504.5	CHAPERONIN HSP78P.	sptrembl O74402	Posttranslational modification, protein turnover, chaperones
7534	500.8	60S RIBOSOMAL PROTEIN L26.	swissnew P78946	Translation, ribosomal structure and biogenesis
7535	499.0	STIL+.	sptrembl O13458	ND
7536	494.4	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE (HOMOLOGY TO UBIQUITIN CARBOXYL-TERMINAL HYDROLASE).	sptrembl Q11119	ND
7537	491.7	HYPOTHETICAL 30.8 KD PROTEIN.	sptrembl O74710	ND
7538	487.5	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP).	swissprot P35691	ND
7539	476.3	DNA BINDING PROTEIN NSDD.	sptrembl Q92226	ND
7540	475.9	60S RIBOSOMAL PROTEIN L34-A.	swissprot P87262	Translation, ribosomal structure and biogenesis
7541	469.2	HYPOTHETICAL 36.7 KD PROTEIN C2E11.10 IN CHROMOSOME I.	sptrembl O14075	ND
7542	460.3	SIMILAR TO ASPARTATE AMINOTRANSFERASE.	sptrembl Q17994	ND
7543	458.0	HYPOTHETICAL 36.7 KD PROTEIN C2F7.14C IN CHROMOSOME I.	swissprot Q09704	Translation, ribosomal structure and biogenesis
7544	455.2	60S RIBOSOMAL PROTEIN L35.	swissprot P17078	Translation, ribosomal structure and biogenesis

7545	439.7	HYPOTHETICAL 53.4 KD PROTEIN (FRAGMENT).	sptrembl Q9Y7E2	ND
7546	438.1	HYPOTHETICAL 59.0 KD PROTEIN C30D11.14 IN CHROMOSOME 1.	swissprot Q09911	ND
7547	435.2	NADPH-DEPENDENT ALDEHYDE REDUCTASE (EC 1.1.1.2) (ALCOHOL DEHYDROGENASE (NADP+)) (ALDEHYDE REDUCTASE (NADPH)).	sptrembl Q12707	ND
7548	428.2	60S RIBOSOMAL PROTEIN L27A (L29).	swissprot P78987	Translation, ribosomal structure and biogenesis
7549	427.9	THIOREDOXIN.	swissprot P42115	ND
7550	420.0	30 KD HEAT SHOCK PROTEIN.	swissprot P19752	ND
7551	418.0	HYPOTHETICAL 25.2 KD PROTEIN.	sptrembl Q9Y7K7	ND
7552	411.8	CALCIUM/PROTON EXCHANGER.	sptrembl O59940	ND
7553	410.0	ASPARTIC PROTEINASE.	sptrembl Q9Y740	ND
7554	409.7	ALPHA,ALPHA-TREHALASE {EC 3.2.1.28}.	tremblnew G1911650	ND
7555	409.4	HYPOTHETICAL 34.2 KD PROTEIN IN CUS1-RPL20A INTERGENIC REGION.	swissprot Q04013	ND
7556	407.7	CARBOXYLIC ACID TRANSPORTER PROTEIN HOMOLOG.	swissprot P36035	ND
7557	402.5	UBIQUITIN-CONJUGATING ENZYME E2-34 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (CELL DIVISION CONTROL PROTEIN 34).	swissprot P14682	ND
7558	400.5	DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE.	tremblnew AAD47296	ND
7559	398.0	NPL1 PROTEIN (SEC63 PROTEIN).	swissprot P14906	Posttranslational modification, protein turnover, chaperones
7560	395.3	HYPOTHETICAL OXIDOREDUCTASE C23D3.11 IN CHROMOSOME I (EC 1.-.-.-).	swissnew Q09851	ND
7561	386.2	HYPOTHETICAL 121.8 KD PROTEIN.	sptrembl O43001	ND
7562	383.9	MDJ1 PROTEIN PRECURSOR.	swissprot P35191	Posttranslational modification, protein turnover, chaperones
7563	383.6	CONSERVED HYPOTHETICAL PROTEIN.	sptrembl O74739	ND
7564	378.5	CELL DIVISION CONTROL PROTEIN 4.	swissprot P53699	ND

7565	366.5	VACUOLAR ATP SYNTHASE SUBUNIT G (EC 3.6.1.34) (V-ATPASE 13 KD SUBUNIT) (VACUOLAR H(+)-ATPASE SUBUNIT G).	swissprot P78713	ND
7566	364.8	VIPI PROTEIN (P53 ANTIGEN HOMOLOG).	sptrembl P87216	ND
7567	359.1	F45H11.2 PROTEIN.	sptrembl Q93725	ND
7568	357.4	CARBONIC ANHYDRASE (EC 4.2.1.1).	sptrembl Q43060	ND
7569	355.5	HYPOTHETICAL 61.3 KD PROTEIN CY369.29.	sptrembl P71838	ND
7570	353.3	ASCOSPORE MATURATION 1 PROTEIN.	sptrembl Q92251	ND
7571	351.2	OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN.	swissprot P07144	ND
7572	350.2	HYPOTHETICAL 30.7 KD PROTEIN IN RVS161-ADP1 INTERGENIC REGION.	swissprot P25613	ND
7573	349.8	HEAT SHOCK FACTOR PROTEIN (HSF) (HEAT SHOCK TRANSCRIPTION FACTOR) (HSTF).	swissprot Q02953	ND
7574	346.1	HYDROXYPROLINE-RICH GLYCOPROTEIN DZ-HRGP PRECURSOR.	tremblnew CAB62280	ND
7575	340.5	W02A2.5 PROTEIN.	sptrembl Q9XUB4	ND
7576	338.3	HYPOTHETICAL 32.6 KD PROTEIN IN VPS15-YMC2 INTERGENIC REGION.	swissprot P38260	ND
7577	337.0	BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE, CYTOSOLIC (EC 2.6.1.42) (BCAT) (TWT2 PROTEIN).	swissprot P47176	ND
7578	336.9	HYPOTHETICAL 34.0 KD PROTEIN IN CTF13-YPK2 INTERGENIC REGION.	swissprot Q03161	ND
7579	330.8	REHYDRIN-LIKE PROTEIN.	sptrembl O94014	ND
7580	329.1	PUTATIVE 20KDA SUBUNIT OF THE V-ATPASE.	sptrembl P87252	ND
7581	328.5	PXP-18.	tremblnew BAA85152	ND
7582	328.0	HYPOTHETICAL 49.6 KD PROTEIN IN ELM1-PRI2 INTERGENIC REGION.	swissprot P36091	ND
7583	326.7	HYDROXYPROLINE-RICH GLYCOPROTEIN DZ-HRGP PRECURSOR.	tremblnew CAB62280	ND
7584	325.9	THIOREDOXIN-LIKE PROTEIN.	tremblnew CAB54816	ND

7585	322.7	PROBABLE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 RNA-BINDING SUBUNIT (EIF-3 RNA-BINDING SUBUNIT) (EIF3 P33) (TRANSLATION INITIATION FACTOR EIF3, P33 SUBUNIT).	swissprot P78795	ND
7586	320.8	MALTOSE PERMEASE.	sptrembl Q9Y845	ND
7587	318.7	HYPOTHETICAL 57.2 KD PROTEIN C12B10.16C IN CHROMOSOME I.	swissprot Q10449	ND
7588	317.3	SOL FAMILY PROTEIN HOMOLOG.	sptrembl O74455	ND
7589	317.2	CLOCK-CONTROLLED GENE-6 PROTEIN.	sptrembl O74694	ND
7590	313.4	PUTATIVE STERIGMATOCYSTIN BIOSYNTHESIS PROTEIN STCT.	swissprot Q00717	ND
7591	311.9	HYPOTHETICAL 92.4 KD PROTEIN.	sptrembl P74690	ND
7592	292.9	PUTATIVE GLUCOSYLTRANSFERASE C17C9.07 (EC 2.4.1.-).	swissprot Q10479	ND
7593	292.5	HYPOTHETICAL 22.0 KD PROTEIN IN FOX3-UBP7 INTERGENIC REGION.	swissprot P40452	ND
7594	288.6	Mutant 2,5-diketo-D-gluconic acid reductase A.	geneseq R49932	ND
7595	282.6	PUTATIVE BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE.	sptrembl Q9Y885	ND
7596	280.5	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).	swissprot Q02817	ND
7597	273.8	CHROMOSOME XV READING FRAME ORF YOL092W.	sptrembl Q12010	ND
7598	273.7	GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE [ISOMERIZING] (EC 2.6.1.16) (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE-6- PHOSPHATE AMIDOTRANSFERASE) (GFAT).	swissprot P53704	ND
7599	272.0	H(+)/MONOSACCHARIDE COTRANSPORTER.	sptrembl O13411	ND
7600	270.1	HYPOTHETICAL 36.8 KD PROTEIN.	sptrembl P71847	ND
7601	269.9	PHOSPHATIDYLETHANOLAMINE N-METHYLTRANSFERASE (EC 2.1.1.17).	swissprot P05374	ND
7602	269.8	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).	swissprot P13983	ND
7603	269.2	HYPOTHETICAL 69.0 KD PROTEIN IN PPX1-RPS4B INTERGENIC REGION.	swissprot P38887	ND
7604	263.9	30 KD HEAT SHOCK PROTEIN.	swissprot P19752	ND

7605	261.4	HYDROXYPROLINE-RICH GLYCOPROTEIN DZ-HRGP PRECURSOR.	tremblnew CAB62280	ND
7606	259.9	Polypeptide fragment encoded by gene 29.	geneseqp Y01464	ND
7607	255.7	Klebsiella pneumoniae glycerol-3-phosphate dehydrogenase.	geneseqp W60255	ND
7608	254.9	HYDROXYPROLINE-RICH GLYCOPROTEIN.	sptrembl Q42366	ND
7609	253.2	Sugar beet chitinase 1.	geneseqp R28150	ND
7610	250.2	THIOREDOXIN-LIKE PROTEIN.	tremblnew CAB54816	ND
7611	247.7	P7 PREINSERTION DNA.	sptrembl Q60501	ND
7612	240.7	PROLINE-RICH CELL WALL PROTEIN.	sptrembl Q39789	ND
7613	240.5	COFILIN.	swissprot P78929	ND
7614	238.5	IUCB.	sptrembl Q9XCH3	ND
7615	238.0	Human actVA-ORF4-like protein sequence.	geneseqp Y14147	ND
7616	233.1	HYDROXYPROLINE-RICH GLYCOPROTEIN DZ-HRGP PRECURSOR.	tremblnew CAB62280	ND
7617	232.3	HYPOTHETICAL 38.8 KD PROTEIN IN MIC1-SRB5 INTERGENIC REGION.	swissprot P53259	ND
7618	232.0	HYPOTHETICAL 41.8 KD PROTEIN (FRAGMENT).	tremblnew CAB55926	ND
7619	231.3	HYPOTHETICAL 22.2 KD PROTEIN IN ERP6-TFG2 INTERGENIC REGION.	swissprot P53200	ND
7620	230.2	WP6 PRECURSOR.	sptrembl Q39492	ND
7621	228.1	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95) (PGDH).	swissprot P73821	ND
7622	225.7	EXTENSIN (FRAGMENT).	sptrembl Q41645	ND
7623	225.5	HYPOTHETICAL PROTEIN MJ1527 PRECURSOR.	sptrembl Q58922	ND
7624	225.3	EXTENSIN (FRAGMENT).	sptrembl Q41645	ND
7625	225.3	CELL DIVISION-ASSOCIATED PROTEIN BIMB.	swissprot P33144	ND
7626	225.0	CYSTEINE-RICH PROTEIN (FRAGMENT).	sptrembl Q16861	ND
7627	223.6	PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C6G9.08 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).	swissprot Q92353	ND

7628	223.0	EPD2 PROTEIN.	sptrembl O74137	ND
7629	221.4	PROLINE-RICH CELL WALL PROTEIN.	sptrembl Q39789	ND
7630	220.5	CHROMOSOME XII COSMID 8167.	sptrembl Q05790	ND
7631	220.4	HYPOTHETICAL PROTEIN C30B4.01C IN CHROMOSOME II (FRAGMENT).	sptrembl P87179	ND
7632	219.3	26S PROTEASOME REGULATORY SUBUNIT.	sptrembl O74762	ND
7633	218.6	NEUROFIBROMATOSIS TYPE I.	sptrembl Q9YGV2	ND
7634	217.6	30 KD HEAT SHOCK PROTEIN.	swissprot P19752	ND
7635	217.6	DNA-DIRECTED RNA POLYMERASE III 36 KD POLYPEPTIDE (EC 2.7.7.6) (C34).	swissprot P32910	ND
7636	217.3	EXTENSIN PRECURSOR (PROLINE- RICH GLYCOPROTEIN).	swissprot P24152	ND
7637	216.9	PROTEOPHOSPHOGLYCAN (FRAGMENT).	sptrembl Q9Y075	ND
7638	214.5	MUCIN (FRAGMENT).	sptrembl Q14888	ND
7639	213.6	HYPOTHETICAL 141.6 KD PROTEIN.	sptrembl O59704	ND
7640	212.3	ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR.	swissprot P01097	ND
7641	209.6	AVICELASE III.	sptrembl O74170	ND
7642	207.1	CYSTEINE SYNTHASE (EC 4.2.99.8) (O-ACETYL SERINE SULFHYDRYLASE) (O- ACETYL SERINE (THIOL)-LYASE) (CSASE).	swissprot P50867	ND
7643	205.8	CHROMOSOME XVI COSMID 9659.	sptrembl Q06505	ND
7644	205.4	EXTENSIN PRECURSOR (PROLINE- RICH GLYCOPROTEIN).	swissprot P14918	ND
7645	204.9	DIMERIC DIHYDRODIOL DEHYDROGENASE (EC 1.3.1.20).	tremblnew BAA83488	ND
7646	204.1	HYPOTHETICAL 29.3 KD PROTEIN (ORF92).	swissprot O10341	ND
7647	203.6	Intestinal mucin deduced from clone SMUC 40.	geneseqp R07670	ND
7648	202.8	PUTATIVE GLUCANASE PRECURSOR.	tremblnew CAB57923	ND
7649	202.7	PDI RELATED PROTEIN A.	sptrembl O93914	ND
7650	202.6	UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN).	swissprot P32626	ND
7651	201.8	HYPOTHETICAL 32.8 KD PROTEIN.	sptrembl O60110	ND
7652	199.7	EXTENSIN-LIKE PROTEIN.	tremblnew CAA22152	ND

7653	199.1	MUCIN (FRAGMENT).	sptrembl Q14887	ND
7654	198.3	HYPOTHETICAL PROTEIN KIAA0107.	swissprot Q15008	ND
7655	197.6	HYDROXYPROLINE-RICH GLYCOPROTEIN DZ-HRGP PRECURSOR.	tremblnew CAB62280	ND
7656	197.3	PIPSQUEAK PROTEIN (ORF-A SHORT).	sptrembl Q24455	ND
7657	196.8	CHA4 ACTIVATORY PROTEIN.	swissprot P43634	ND
7658	195.7	PUTATIVE ALPHA,ALPHA-TREHALOSE-PHOSPHATE SYNTHASE.	tremblnew CAB52715	ND
7659	193.6	NEURON-DERIVED ORPHAN RECEPTOR-1 BETA.	sptrembl O97727	ND
7660	193.5	HYDROXYPROLINE-RICH GLYCOPROTEIN PRECURSOR.	sptrembl Q41719	ND
7661	193.4	SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).	swissprot Q01130	ND
7662	193.0	ALPHA/BETA-GLIADIN CLONE PW1215 PRECURSOR (PROLAMIN).	swissprot P04726	ND
7663	193.0	ORF-3.	sptrembl Q01823	ND
7664	192.1	SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).	swissprot P21997	ND
7665	191.8	RNA BINDING PROTEIN (FRAGMENT).	tremblnew BAA83714	ND
7666	191.1	PUTATIVE PROLINE-RICH PROTEIN.	sptrembl Q9ZW08	ND
7667	190.8	NAPG OXIDOREDUCTASE.	sptrembl Q9X653	ND
7668	190.0	EXTENSIN (FRAGMENT).	sptrembl Q41645	ND
7669	189.5	NADH-UBIQUINONE OXIDOREDUCTASE 21 KD SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-21KD) (CI-21KD).	swissprot Q02854	ND
7670	188.9	SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.	swissprot P02840	ND
7671	188.3	DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN GLYCOSYLTRANSFERASE ALPHA SUBUNIT PRECURSOR (EC 2.4.1.119) (OLIGOSACCHARYL TRANSFERASE ALPHA SUBUNIT) (OLIGOSACCHARYL TRANSFERASE 64 KD SUBUNIT).	swissprot P41543	ND
7672	188.2	CDC-LIKE PROTEIN (FRAGMENT).	sptrembl O08837	ND
7673	186.3	PUTATIVE PROLINE-RICH PROTEIN.	sptrembl Q9ZW08	ND

7674	186.3	HYDROLASE 434 aa, chain A+B	pdb 4CEL	ND
7675	185.9	SPLICING COACTIVATOR SUBUNIT SRM300.	tremblnew AAF21439	ND
7676	184.3	HEAT SHOCK PROTEIN-LIKE PROTEIN.	sptrembl O23323	ND
7677	183.9	PLENTY-OF-PROLINES-101.	sptrembl O70495	ND
7678	183.3	PROLINE-RICH SALIVARY PROTEIN (FRAGMENT).	sptrembl Q62107	ND
7679	181.6	SUGAR TRANSPORTER, PUTATIVE.	tremblnew AAF12486	ND
7680	180.8	KIAA0775 PROTEIN.	sptrembl O94873	ND
7681	179.8	GAMMA GLIADIN (FRAGMENT).	sptrembl Q41602	ND
7682	179.6	HYPOTHETICAL 61.1 KD PROTEIN (FRAGMENT).	tremblnew CAB63715	ND
7683	179.4	NADH-UBIQUINONE OXIDOREDUCTASE 21 KD SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-21KD) (CI-21KD).	swissprot Q02854	ND
7684	179.2	PROLINE-RICH CELL WALL PROTEIN.	sptrembl Q39763	ND
7685	178.1	Amino acid sequence of a virulence factor encoded by ORF25510.	geneseqp Y29194	ND
7686	176.8	HYPOTHETICAL 47.5 KD PROTEIN IN APE3-APM3 INTERGENIC REGION.	swissprot P38355	ND
7687	176.8	LOW MOLECULAR WEIGHT GLUTENIN (FRAGMENT).	sptrembl Q41550	ND
7688	176.2	HYPOTHETICAL 57.2 KD PROTEIN.	sptrembl O68872	ND
7689	175.9	TIG11.14 PROTEIN.	sptrembl O23024	ND
7690	175.4	GLYCOLIPID ANCHORED SURFACE PROTEIN PRECURSOR (GLYCOPROTEIN GPI15).	swissprot P22146	ND
7691	175.1	Bioadhesive precursor protein from cDNA 52.	geneseqp P82971	ND
7692	175.0	PISTIL EXTENSIN-LIKE PROTEIN.	sptrembl Q40385	ND
7693	174.7	PROLINE-RICH PROTEOGLYCAN PRPG2.	sptrembl Q07611	ND
7694	174.7	Antibiotic potentiating peptide #3.	geneseqp W21591	ND
7695	174.7	HOMEBOX PROTEIN MOX-2 (GROWTH ARREST-SPECIFIC HOMEBOX).	swissprot P39020	ND
7696	173.6	REPETIN.	swissprot P97347	ND
7697	172.9	PROTEOPHOSPHOGLYCAN (FRAGMENT).	sptrembl Q9Y075	ND
7698	172.6	Sugar beet chitinase 1.	geneseqp R28150	ND

7699	172.1	FORMYLTETRAHYDROFOLATE DEFORMYLASE (EC 3.5.1.10) (FORMYL-FH(4) HYDROLASE).	swissprot Q46339	ND
7700	171.9	HYPOTHETICAL 23.2 KD PROTEIN.	sptrembl O41979	ND
7701	170.6	CORTICOTROPIN RELEASING HORMONE RECEPTOR TYPE I (FRAGMENT).	sptrembl O77677	ND
7702	170.3	31-KDA PROLINE-RICH SALIVARY PROTEIN, COMPLETE CDS OF CLONE PUM125.	sptrembl Q62105	ND
7703	169.6	BLUE-COPPER BINDING PROTEIN III.	sptrembl Q96316	ND
7704	169.0	D9461.20P.	sptrembl Q04080	ND
7705	168.8	50KD PROLINE RICH PROTEIN.	sptrembl Q9ZBP2	ND
7706	168.3	FLGA insert stabilising polypeptide.	geneseqp W79128	ND
7707	168.1	VRG53 PROTEIN (FRAGMENT).	sptrembl Q05844	ND
7708	168.0	Mycobacterium species protein sequence 5C.	geneseqp Y04773	ND
7709	167.8	CHAPERONIN HSP78P.	sptrembl O74402	ND
7710	167.0	Microtubule-associated tau protein epitope corresp. to pos. 146-251.	geneseqp R92516	ND
7711	166.2	SPLICING FACTOR SRP54.	sptrembl O61646	ND
7712	166.1	Fragmented human NF-H gene +2 frameshift mutant product.	geneseqp W18663	ND
7713	166.0	Amino acid sequence of Huntington's gene exon 1 in GST-HD fusion protein.	geneseqp W95071	ND
7714	165.8	BIFID PROTEIN (OPTOMOTOR-BLIND PROTEIN).	sptrembl Q26303	ND
7715	165.6	212AA LONG HYPOTHETICAL PROTEIN.	sptrembl Q9YEG1	ND
7716	164.5	Amino acid sequence of a virulence factor encoded by ORF31784.	geneseqp Y29225	ND
7717	164.4	SIMILAR TO CUTICULAR COLLAGEN.	sptrembl Q19813	ND
7718	164.4	Amino acid sequence of a virulence factor encoded by ORF32832.	geneseqp Y29230	ND
7719	164.2	ZINC-FINGER PROTEIN.	sptrembl O74308	ND
7720	163.9	BAT2.	sptrembl Q9Z1R1	ND
7721	163.7	PAD-1.	sptrembl Q9Y7A8	ND
7722	163.3	TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2) (HFK2).	swissprot P55316	ND
7723	163.2	HYPOTHETICAL 27.0 KD PROTEIN.	sptrembl P95286	ND
7724	163.0	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.	swissprot P32323	ND

7725	162.4	Trichoderma reesei endoglucanase.	geneseqp R83401	ND
7726	162.1	T12F5.5 PROTEIN.	sptrembl O44760	ND
7727	162.0	RNA BINDING PROTEIN (FRAGMENT).	tremblnew BAA83717	ND
7728	161.9	TRANSDUCIN-LIKE ENHANCER PROTEIN 4 (GROUCHO-RELATED PROTEIN 4) (FRAGMENT).	swissnew Q62441	ND
7729	161.5	Mycobacterium species protein sequence 14Q#2.	geneseqp Y07202	ND
7730	161.3	SWI/SNF COMPLEX 170 KDA SUBUNIT.	sptrembl Q92923	ND
7731	161.1	HIV Tat protein.	geneseqp Y05097	ND
7732	160.7	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.	swissprot P47179	ND
7733	160.6	COMES FROM THIS GENE.	sptrembl O23054	ND
7734	160.6	PYRUVATE DEHYDROGENASE E1 COMPONENT ALPHA SUBUNIT (EC 1.2.4.1) (PYRUVATE DEHYDROGENASE (LIPOAMIDE)) (PYRUVATE DECARBOXYLASE) (PYRUVIC DEHYDROGENASE).	sptrembl O13392	ND
7735	160.6	GLYCINE-RICH PROTEIN.	sptrembl Q43308	ND
7736	160.5	METHYLTRANSFERASE.	sptrembl Q51774	ND
7737	160.4	RHBA.	tremblnew AAF24249	ND
7738	160.3	ULTRA-HIGH SULPHUR KERATIN.	sptrembl Q64526	ND
7739	160.2	PROLYL AMINOPEPTIDASE.	sptrembl P94800	ND
7740	159.9	HOMEBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN- SPECIFIC HOMEBOX PROTEIN 2).	swissprot P52951	ND
7741	159.6	PUTATIVE MEMBRANE PROTEIN.	sptrembl Q9X780	ND
7742	159.4	Human secreted protein encoded by gene 41c lone HSZAF47.	geneseqp Y02690	ND
7743	159.0	Human apolipoprotein E gene +2 frameshift mutant product.	geneseqp W18652	ND
7744	158.6	HYPOTHETICAL 9.0 KD PROTEIN (FRAGMENT).	sptrembl Q9XSS3	ND
7745	158.4	ORF993.	sptrembl P72344	ND
7746	158.2	ORF1B.	sptrembl Q47393	ND
7747	157.7	SMR2 PROTEIN PRECURSOR.	swissprot P18897	ND
7748	157.5	RECOMBINATION PROTEIN RECR.	swissprot P24277	ND

7749	157.3	Human alpha 5 (IV) of type IV collagen.	geneseqp R23873	ND
7750	157.1	PROLINE-RICH PROTEIN.	tremblnew CAB62486	ND
7751	156.5	GAMMA PROTEIN CONSTANT REGION (FRAGMENT).	sptrembl Q23723	ND
7752	156.1	NK-TUMOR RECOGNITION MOLECULE-RELATED PROTEIN.	sptrembl O43273	ND
7753	155.6	SPLICING FACTOR, ARGININE/SERINE-RICH 7 (SPLICING FACTOR 9G8).	swissnew Q16629	ND
7754	154.3	ACETYLCHOLINESTERASE-ASSOCIATED COLLAGEN (FRAGMENT).	sptrembl O35348	ND
7755	153.8	PROBABLE PROTEIN KINASE.	tremblnew CAB55520	ND
7756	153.6	Human high mobility group protein HMGI-C wild type fragment 2.	geneseqp Y21432	ND
7757	153.6	NANBH virus antigenic fragment #12.	geneseqp R50080	ND
7758	153.6	Del-1 epidermal growth factor like domain #2.	geneseqp W94687	ND
7759	153.5	SH3 DOMAIN BINDING PROTEIN.	sptrembl Q62775	ND
7760	153.3	COLLAGEN ALPHA 5(IV) CHAIN (FRAGMENT).	swissprot Q28247	ND
7761	153.0	SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.	swissprot P13729	ND
7762	152.5	MRNA EXPRESSED IN CUCUMBER HYPOCOTYLS, COMPLETE CDS.	sptrembl Q9XIV1	ND
7763	152.4	PROTEOPHOSPHOGLYCAN PRECURSOR (FRAGMENT).	sptrembl Q9Y076	ND
7764	152.3	ARL-6 INTERACTING PROTEIN-5 (FRAGMENT).	sptrembl Q9WUG9	ND
7765	150.4	HYPOTHETICAL 70.4 KD PROTEIN IN SNZ1-YPK2 INTERGENIC REGION.	swissprot Q03153	ND
7766	150.3	L779.3 PROTEIN.	sptrembl Q9XTP1	ND
7767	150.3	Fragment of human secreted protein encoded by gene 15.	geneseqp Y36459	ND
7768	150.3	HOX1B PROTEIN.	sptrembl O24569	ND
7769	149.8	HYPOTHETICAL 13.9 KD PROTEIN.	tremblnew AAF19661	ND
7770	149.7	Mycobacterium species protein sequence 50B.	geneseqp Y04998	ND
7771	149.6	T06E4.11 PROTEIN.	sptrembl Q22265	ND
7772	148.8	Avian reovirus strain 138 sigma 3 protein.	geneseqp Y06109	ND
7773	148.3	GSC-2.	sptrembl O15499	ND
7774	148.2	CODED FOR BY C. ELEGANS CDNA YK127B8.5.	sptrembl Q20648	ND

7775	147.8	ORF225.	sptrembl Q44479	ND
7776	146.8	WD-40 domain-contg. TUP1 homolog protein.	geneseqp R85879	ND
7777	146.8	EN/SPM-LIKE TRANSPOSON PROTEIN.	tremblnew AAD20682	ND
7778	146.5	PROLINE RICH PROTEIN.	sptrembl O22514	ND
7779	146.4	Secreted protein encoded by gene 6 clone HTSEW17.	geneseqp Y01388	ND
7780	146.3	HOMEODOMAIN PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEODOMAIN PROTEIN 2).	swissprot P52951	ND
7781	145.6	NUCLEOPLASMIN.	swissnew P05221	ND
7782	145.3	TYROSINE-PROTEIN KINASE ACK (EC 2.7.1.112).	sptrembl Q07912	ND
7783	144.9	INTEGRIN BETA-SUBUNIT.	sptrembl Q27874	ND
7784	144.2	SIMILARITY WITH WILMS' TUMOR PROTEIN.	sptrembl Q18233	ND
7785	143.5	F25965_3.	sptrembl O14560	ND
7786	142.5	HYPOTHETICAL 38.0 KD PROTEIN.	sptrembl O06232	ND
7787	142.5	DAN26 PROTEIN, PARTIAL (FRAGMENT).	sptrembl Q99492	ND
7788	142.2	ATTACHMENT REGION BINDING PROTEIN (FRAGMENT).	sptrembl O42403	ND
7789	142.1	S-LAYER RELATED PROTEIN PRECURSOR.	swissprot P35824	ND
7790	141.9	NONSTRUCTURAL POLYPROTEIN (FRAGMENT).	sptrembl Q9W181	ND
7791	141.9	ATTI.	sptrembl Q9WWD7	ND
7792	141.3	ENDOGLUCANASE IV.	sptrembl O14405	ND
7793	141.1	GAMMA-GLIADIN PRECURSOR (FRAGMENT).	swissprot P08079	ND
7794	140.9	Mycobacterium species protein sequence 36B.	geneseqp Y04923	ND
7795	140.9	VPR.	sptrembl O90320	ND
7796	140.8	NUCLEAR ANTIGEN EBNA-3B.	sptrembl Q69139	ND
7797	140.4	TRANSCRIPTIONAL ACTIVATOR PROTEIN METR.	swissprot P19797	ND
7798	140.4	CALCIUM-DEPENDENT PROTEIN KINASE.	sptrembl O82107	ND
7799	139.1	(HHV-6).	sptrembl Q89893	ND
7800	139.1	HYPOTHETICAL 12.0 KD PROTEIN (FRAGMENT).	sptrembl O43409	ND
7801	138.9	SMAD6 PROTEIN.	tremblnew AAF14343	ND

7802	138.9	ARGININE/SERINE-RICH PROTEIN.	tremblnew AAF19004	ND
7803	138.8	107AA LONG HYPOTHETICAL PROTEIN.	sptrembl Q9YCW7	ND
7804	137.9	Human fibrosarcoma cell line HT-1080 clone HP10034 protein.	geneseqp W64540	ND
7805	137.9	Extracellular domain of mouse syndecan-3 protein.	geneseqp R66810	ND
7806	137.8	SIMILAR TO FURIN-LIKE PROTEASES.	sptrembl Q93015	ND
7807	137.7	PROTEASOME COMPONENT SUN4.	swissprot P53616	ND
7808	137.6	HYPOTHETICAL 26.9 KD PROTEIN.	tremblnew AAF10289	ND
7809	137.2	HYPOTHETICAL 22.1 KD PROTEIN.	sptrembl P94570	ND
7810	137.1	WINGLESS (FRAGMENT).	tremblnew AAD50945	ND

Example 15: DNA Microarrays

Details of the construction of a typical microarrayer can be found on the world wide web site of Professor Patrick Brown of Stanford University at the following URL:

- 5 <http://cmgm.stanford.edu/pbrown/mguide/index.html>. Scanners and computer software for analysis of DNA microarrays are available from several commercial sources such as General Scanning Inc. (Watertown, MA; see http://www.genscan.com/sales/loc_lifesci.html), or Axon Instruments (Foster City, CA; see <http://www.axon.com>).

- 10 Individual fungal EST clones were purified as plasmid minipreps using Qiagen Biorobot 9600 (QIAGEN, Inc., Valencia, CA). The plasmid minipreps were precipitated with isopropanol, aliquoted and stored as described on the web site of Professor Patrick Brown of Stanford University at the following URL: <http://cmgm.stanford.edu/pbrown/mguide/index.html>.

- 15 The amplified EST targets prepared in this manner were spotted individually onto polylysine-coated glass slides using a microarrayer device as described by DeRisi *et al.* (1997, *Science* 278: 680-686). For additional details, see <http://cmgm.stanford.edu/pbrown/protocols/index.html>). The microarrays were probed with fluorescently labeled cDNA prepared by reverse transcription of polyadenylated
20 mRNA (DeRisi *et al.*, 1997, *supra*) extracted from fungal mycelia (Example 2). Conditions for pretreatment of the microarrays, hybridization and washing conditions have been described previously (DeRisi *et al.*, 1997, *supra*; see also

<210> 7521
<211> 807
<212> DNA
<213> Tricoderma reesei

<220>
<221> misc_feature
<222> (1)...(807)
<223> n = A,T,C or G

<400> 7521
actctctagc tgaacaaatt atctgcgcaa acatgggttcg cgggactgct ctgctggccc 60
ttggggctct ctcaacgctc tatatggccc aaatctcaga cgacttcgag tcgggctggg 120
atcagactaa atggcccatt tcggcaccag actgtaacca gggcggcacc gtcagcctcg 180
acaccacagt agcccacagc ggcagcaact ccatgaaggt cggtgggtggc cccaatggct 240
actgtggaca catcttcttc ggcactaccc aggtgccaac tggggatgta tatgtcagag 300
cttggattcg gcttcagact gctctcggca gcaaccacgt cacattcatc atcatgccag 360
acaccgntca gggaggggaag cacttcgaa ttgggtggcca aagccaagtt ctcgactaca 420
accgcgagtc cgacgatgcc actcttcggg acctgtctcc caacggcatt gcctccaccg 480
tcactctgct accnggcgcc gttccagtgc ttcnagtacc acctgggcac ttgacggaac 540
catcgagacg tggctcaacg gcagntcat ccggggcatg accgtgggccc ctggcgctcgn 600
acaatccaaa cgacgcttgg cttggacgaa gggccaagct tttatttccg gagatcaccg 660
gtgtcaactt ttggcttggg anggcctaca gcgganacgt aaacaacccg tctgggtcga 720
ngacatctcg attngtgcga ccnngcgtgg gatgcggccc cggcagcccc ggcggtcctg 780
gaagctcgac gactgggcna ngcagca 807

<210> 7522
<211> 413
<212> DNA
<213> Tricoderma reesei

<220>
<221> misc_feature
<222> (1)...(413)
<223> n = A,T,C or G

<400> 7522
acaaccagac gatcatcagc aaccacttcc gcaaggattg gcagagacgg gttcgcaccc 60
actttgacca gcccggccga aagtctcgga gacgcactgc tcgtcaggcc aaggctgctg 120
ccctcgctcc tcgtcccgtc gacaagctgc gcccgctcgt gcgatgccct accattaggt 180
acaaccgccc ggtccgcgcc ggtcgtgggt tcacctcac cgagctcaag gaggcgggta 240
tctccaagtc cctggctccc accatcggca tcgcccgcga cttccgcgcg cagaacctga 300
gcgaggagaa gcctngccgc caacgtggcc cgctcaaggc ctacaaagga gcgcctcatc 360
ctctgcccgc aagtccaacg cccnaagaa ggggtgacacc angaccgacg tct 413

<210> 7523
<211> 588
<212> DNA
<213> Tricoderma reesei

<220>
<221> misc_feature
<222> (1)...(588)
<223> n = A,T,C or G

<400> 7523
atccaggcct ggtacggcgg naacgagacg ggcaactcca ttgccgacgt cgtctttggc 60
gactacaacc cctcgggcaa gctgtccctc agcttcccca agcgcctgca ggacaacccc 120
gcgtttctca acttccgcac cgaggccggg cgacgctgt acggcgagga cgtctacgtc 180

92.8% match
local similarity

```

gggtacaggt actacgagtt tgccgacaag gacgtcaatt tcccccttgg ccacggcctg 240
tcctacacca ctttttgcct ttttccaatc tcttccgggg tcttaacaan ggacggnaaa 300
gcttgaagcc gtggttccct ntccgngga aagaaacaac cnggcttcng tgcccnggc 360
gcaacaaggt ggggccaag ctntttacgt taaagcnc ctcnaagcc gggccaagaa 420
atnaanccgg ccccggtcaa nggagcttna aaggggcttt tcgcaaaaagg gtcgaactgg 480
caagcccccg ggggaaaaac naaaggncgg gngaacaatt cganggagcc anggaanaaa 540
gtnccggttcn cttnggtat ttttgatgn aaggaagccg gggaatca 588

```

<210> 7524

<211> 768

<212> DNA

<213> Tricoderma reesei

<220>

<221> misc_feature

<222> (1) ... (768)

<223> n = A,T,C or G

<400> 7524

```

ctatctcctt cgtcctctcc ctacttgaca cattcttctt tctcctgccc ccctcttttt 60
ccggcttgcg cagctctctt cttcgccctc cgcgctcgcc gcatcgactc tcaatttcca 120
gtttccaggc agtcgcgcgt ctaagccaca gcgctggtct gtgtcgcaac tcttgccaac 180
atgtcggacc atgagtttgg cggaagcaac gatgacctat cgctgcaaaa gctaccgttc 240
agaagattgt cagcgaataa ttgccaccgc agacaggcgt ctntttcgca aggaggctcg 300
tgacctgctc atagaatgct gtgtcgagtt catcaccctn atcttgctcg aggccaacga 360
gatcttngag aaggaagcga aaaagaccat tgctcgacac cacataccaa ggcgctagaa 420
cgcttgggct tttccgacta cgtgcccgcg gtgtggagg cgccggccga acacaaggaa 480
acgcaaaaagg ggcgagagaa aaaggcagac aagtttgcca acaagcgggc tgtctatgga 540
ggagctcgct cggctgcagg aaagcaattc gncgcggnc aacagcgcca cacatgatgg 600
aatttgcttt tttctttttt cttttcngtg atattggggg ggaagaaggc gtcacacggg 660
gggcattact aggcgtttta tacacgggtg gtgagggttg gtaaggtaac aggtcagact 720
tttttgattt gggccttcat tccccggagt nggttnttaa gttatatt 768

```

<210> 7525

<211> 729

<212> DNA

<213> Tricoderma reesei

<220>

<221> misc_feature

<222> (1) ... (729)

<223> n = A,T,C or G

<400> 7525

```

aaggcaattc ctctgggctc catcaaattc attggtacct ccacagcgca ggatgactgg 60
ttctcactgg gcatcgatc tccgcaggaa gcagaccctc ttatgaactg cgtgttcaag 120
acggaaatgt ttaccagat gcagcgtgcc atgccgggag gcttcaacct caagatcggc 180
gagacgattg aatacgcaaa gaagccgggc aagatgcagc angtcaaggt tctcaaggac 240
tctcagcagc gggctgacta ctacaagagc ggcgcgatcc acacgcagcc aggagagcct 300
ccaaattcgg tatcaaagcc gatgcccagg gccaaagccc tgccgcgcgc gccatcacca 360
gaggcaagct catcaagccc ggtggtncgg gaggcaggcc gtccagaatc accgccaccc 420
gcaacactca gccgagatca acgggcaccg gtaccaggag cgttctccgc cgccgccggt 480
cttggtggca tagtatcgga tcatcatcgg cctcatcgaa cgcggggccc tcggcaagca 540
caagcacatt gagctcgctg acgcatcaaa tccccgttgt cggaatgcc ataaccggtc 600
naacagcccc ccagaaacca gtcaggcagc gctngacgcc gcttcttcgc cgcccttctt 660
gnccttctgn tgtaagcca anatatggcc aagngtata tnattctccn gccagaagga 720
aacgacttg

```

<210> 7526

<211> 471

Claims

What is claimed is:

- 5 1. A method for monitoring differential expression of a plurality of genes in a first filamentous fungal cell relative to expression of the same genes in one or more second filamentous fungal cells, comprising:
- (a) adding a mixture of fluorescence-labeled nucleic acids isolated from the filamentous fungal cells to a substrate containing an array of filamentous fungal ESTs
10 under conditions where the nucleic acids hybridize to complementary sequences of the ESTs in the array, wherein the nucleic acids from the first filamentous fungal cell and the one or more second filamentous fungal cells are labeled with a first fluorescent reporter and one or more different second fluorescent reporters, respectively; and
- (b) examining the array by fluorescence under fluorescence excitation conditions
15 wherein the relative expression of the genes in the filamentous fungal cells is determined by the observed fluorescence emission color of each spot in the array in which (i) the ESTs in the array that hybridize to the nucleic acids obtained from either the first or the one or more second filamentous fungal cells produce a distinct first fluorescence emission color or one or more second fluorescence emission colors, respectively, and (ii)
20 the ESTs in the array that hybridize to the nucleic acids obtained from both the first and one or more second filamentous fungal cells produce a distinct combined fluorescence emission color.
2. The method of claim 1, wherein the filamentous fungal ESTs are selected from
25 the group consisting of *Acremonium*, *Aspergillus*, *Fusarium*, *Humicola*, *Mucor*, *Myceliophthora*, *Neurospora*, *Penicillium*, *Thielavia*, *Tolypocladium*, and *Trichoderma* ESTs.
3. The method of claim 2, wherein the filamentous fungal ESTs are *Fusarium* ESTs.
30
4. The method of claim 3, wherein the filamentous fungal ESTs are *Fusarium venenatum* ESTs.

5. The method of claim 4, wherein the *Fusarium venenatum* ESTs are selected from the group consisting of SEQ ID NOs. 1-3770, nucleic acid fragments of SEQ ID NOs. 1-3770, and nucleic acid sequences having at least 90% homology to SEQ ID NOs. 1-3770.
- 5 6. The method of claim 5, wherein the *Fusarium venenatum* ESTs are SEQ ID NOs. 1-3770.
7. The method of claim 5, wherein the *Fusarium venenatum* ESTs are nucleic acid
10 sequences having at least 90% homology to SEQ ID NOs. 1-3770.
8. The method of claim 7, wherein the *Fusarium venenatum* ESTs are nucleic acid sequences having at least 95% homology to SEQ ID NOs. 1-3770.
- 15 9. The method of claim 8, wherein the *Fusarium venenatum* ESTs are nucleic acid sequences having at least 99% homology to SEQ ID NOs. 1-3770.
10. The method of claim 9, wherein the *Fusarium venenatum* ESTs are nucleic acid sequences having at least 99.9% homology to SEQ ID NOs. 1-3770.
- 20 11. The method of claim 2, wherein the filamentous fungal ESTs are *Aspergillus* ESTs.
12. The method of claim 11, wherein the *Aspergillus* ESTs are *Aspergillus niger*
25 ESTs.
13. The method of claim 12, wherein the *Aspergillus niger* ESTs are selected from the group consisting of SEQ ID NOs. 3771-4376, nucleic acid fragments of SEQ ID NOs. 3771-4376, and nucleic acid sequences having at least 90%, preferably at least
30 95%, more preferably at least 99%, and most preferably at least 99.9% homology to SEQ ID NOs. 3771-4376.

14. The method of claim 13, wherein the *Aspergillus niger* ESTs are SEQ ID NOs. 3771-4376.
15. The method of claim 13, wherein the *Aspergillus niger* ESTs are nucleic acid sequences having at least 90% homology to SEQ ID NOs. 3771-4376.
16. The method of claim 15, wherein the *Aspergillus niger* ESTs are nucleic acid sequences having at least 95% homology to SEQ ID NOs. 3771-4376.
17. The method of claim 16, wherein the *Aspergillus niger* ESTs are nucleic acid sequences having at least 99% homology to SEQ ID NOs. 3771-4376.
18. The method of claim 17, wherein the *Aspergillus niger* ESTs are nucleic acid sequences having at least 99.9% homology to SEQ ID NOs. 3771-4376.
19. The method of claim 11, wherein the *Aspergillus* ESTs are *Aspergillus oryzae* ESTs.
20. The method of claim 19, wherein the *Aspergillus oryzae* ESTs are selected from the group consisting of SEQ ID NOs. 4377-7401, nucleic acid fragments of SEQ ID NOs. 4377-7401, and nucleic acid sequences having at least 90% homology to SEQ ID NOs. 4377-7401.
21. The method of claim 20, wherein the *Aspergillus oryzae* ESTs are SEQ ID NOs. 4377-7401.
22. The method of claim 20, wherein the *Aspergillus oryzae* ESTs are nucleic acid sequences having at least 90% homology to SEQ ID NOs. 4377-7401.
23. The method of claim 22, wherein the *Aspergillus oryzae* ESTs are nucleic acid sequences having at least 95% homology to SEQ ID NOs. 4377-7401.

24. The method of claim 23, wherein the *Aspergillus oryzae* ESTs are nucleic acid sequences having at least 99% homology to SEQ ID NOs. 4377-7401.
25. The method of claim 24, wherein the *Aspergillus oryzae* ESTs are nucleic acid sequences having at least 99.9% homology to SEQ ID NOs. 4377-7401.
26. The method of claim 2, wherein the filamentous fungal ESTs are *Trichoderma* ESTs.
27. The method of claim 26, wherein the filamentous fungal ESTs are *Trichoderma reesei* ESTs.
28. The method of claim 27, wherein the *Trichoderma reesei* ESTs are selected from the group consisting of SEQ ID NOs. 7402-7860, nucleic acid fragments of SEQ ID NOs. 7402-7860, and nucleic acid sequences having at least 90% homology to SEQ ID NOs. 7402-7860.
29. The method of claim 28, wherein the *Trichoderma reesei* ESTs are SEQ ID NOs. 7402-7860.
30. The method of claim 28, wherein the *Trichoderma reesei* ESTs are nucleic acid sequences having at least 90% homology to SEQ ID NOs. 7402-7860.
31. The method of claim 30, wherein the *Trichoderma reesei* ESTs are nucleic acid sequences having at least 95% homology to SEQ ID NOs. 7402-7860.
32. The method of claim 31, wherein the *Trichoderma reesei* ESTs are nucleic acid sequences having at least 99% homology to SEQ ID NOs. 7402-7860.
33. The method of claim 32, wherein the *Trichoderma reesei* ESTs are nucleic acid sequences having at least 99.9% homology to SEQ ID NOs. 7402-7860.

34. The method of any of claims 1-33, wherein one or more of filamentous fungal cells are selected from the group consisting of an *Acremonium*, *Aspergillus*, *Fusarium*, *Humicola*, *Mucor*, *Myceliophthora*, *Neurospora*, *Penicillium*, *Thielavia*, *Tolypocladium*, and *Trichoderma* cell.
- 5
35. The method of any of claims 1-34, wherein the two or more filamentous fungal cells are the same cell.
36. The method of any of claims 1-35, wherein the two or more filamentous fungal
10 cells are *Fusarium venenatum* cells.
37. The method of any of claims 1-35, wherein the two or more filamentous fungal cells are *Aspergillus niger* cells.
- 15 38. The method of any of claims 1-35, wherein the two or more filamentous fungal cells are *Aspergillus oryzae* cells.
39. The method of any of claims 1-34, wherein the two or more filamentous fungal cells are different cells.
- 20
40. The method of any of claims 1-39, wherein the hybridization conditions are selected from the group consisting of very low, low, low-medium, medium, medium-high, high, and very high stringency conditions.
- 25 41. A computer readable medium having recorded thereon an array of filamentous fungal ESTs for monitoring differential expression of a plurality of genes in a first filamentous fungal cell relative to expression of the same genes in one or more second filamentous fungal cells.
- 30 42. The computer readable medium of claim 41, wherein the filamentous fungal ESTs are selected from the group consisting of *Acremonium*, *Aspergillus*, *Fusarium*, *Humicola*, *Mucor*, *Myceliophthora*, *Neurospora*, *Penicillium*, *Thielavia*, *Tolypocladium*,

and *Trichoderma* ESTs.

43. The computer readable medium of claim 42, wherein the filamentous fungal ESTs are *Fusarium* ESTs.

5

44. The computer readable medium of claim 43, wherein the filamentous fungal ESTs are *Fusarium venenatum* ESTs.

45. The computer readable medium of claim 44, wherein the *Fusarium venenatum* ESTs are selected from the group consisting of SEQ ID NOs. 1-3770, nucleic acid fragments of SEQ ID NOs. 1-3770, and nucleic acid sequences having at least 90% homology to SEQ ID NOs. 1-3770.

46. The computer readable medium of claim 45, wherein the *Fusarium venenatum* ESTs are SEQ ID NOs. 1-3770.

15

47. The computer readable medium of claim 45, wherein the *Fusarium venenatum* ESTs are nucleic acid sequences having at least 90% homology to SEQ ID NOs. 1-3770.

48. The computer readable medium of claim 42, wherein the filamentous fungal ESTs are *Aspergillus* ESTs.

20

49. The computer readable medium of claim 48, wherein the *Aspergillus* ESTs are *Aspergillus niger* ESTs.

25

50. The computer readable medium of claim 49, wherein the *Aspergillus niger* ESTs are selected from the group consisting of SEQ ID NOs. 3771-4376, nucleic acid fragments of SEQ ID NOs. 3771-4376, and nucleic acid sequences having at least 90% homology to SEQ ID NOs. 3771-4376.

30

51. The computer readable medium of claim 50, wherein the *Aspergillus niger* ESTs are SEQ ID NOs. 3771-4376

52. The computer readable medium of claim 50, wherein the *Aspergillus niger* ESTs are nucleic acid sequences having at least 90% homology to SEQ ID NOs. 3771-4376.
- 5 53. The computer readable medium of claim 48, wherein the *Aspergillus* ESTs are *Aspergillus oryzae* ESTs.
54. The computer readable medium of claim 53, wherein the *Aspergillus oryzae* ESTs are selected from the group consisting of SEQ ID NOs. 4377-7401, nucleic acid
10 fragments of SEQ ID NOs. 4377-7401, and nucleic acid sequences having at least 90% homology to SEQ ID NOs. 4377-7401.
55. The computer readable medium of claim 54, wherein the *Aspergillus niger* ESTs are SEQ ID NOs. 4377-7401.
- 15 56. The computer readable medium of claim 54, wherein the *Aspergillus oryzae* ESTs are nucleic acid sequences having at least 90% homology to SEQ ID NOs. 4377-7401.
57. The computer readable medium of claim 42, wherein the filamentous fungal
20 ESTs are *Trichoderma* ESTs.
58. The computer readable medium of claim 57, wherein the filamentous fungal ESTs are *Trichoderma reesei* ESTs.
- 25 59. The computer readable medium of claim 58, wherein the *Trichoderma reesei* ESTs are selected from the group consisting of SEQ ID NOs. 7402-7860, nucleic acid fragments of SEQ ID NOs. 7402-7860, and nucleic acid sequences having at least 90% homology to SEQ ID NOs. 7402-7860.
- 30 60. The computer readable medium of claim 59, wherein the *Trichoderma reesei* ESTs are SEQ ID NOs. 7402-7860.

61. The computer readable medium of claim 59, wherein the *Trichoderma reesei* ESTs are nucleic acid sequences having at least 90% homology to SEQ ID NOs. 7402-7860.

5 62. The computer readable medium of any of claims 41-61, wherein the medium is selected from the group consisting of a floppy disk, a hard disk, random access memory (RAM), read only memory (ROM), and CD-ROM.

63. A computer-based system for monitoring differential expression of a plurality of
10 genes in a first filamentous fungal cell relative to expression of the same genes in one or more second filamentous fungal cells comprising the following elements:

(a) a data storage means comprising filamentous fungal ESTs selected from the group consisting of SEQ ID NOs. 1-7860, nucleic acid fragments of SEQ ID NOs. 1-7860, and nucleic acid sequences having at least 90% homology
15 to the sequences of SEQ ID NOs. 1-7860;

(b) a search means for comparing a target sequence to a filamentous fungal EST sequence of the data storage means of step (a) to identify homologous sequences; and

(c) a retrieval means for obtaining the homologous sequence(s) of step
20 (b).

64. A substrate comprising an array of filamentous fungal ESTs for monitoring differential expression of a plurality of genes in a first filamentous fungal cell relative to expression of the same genes in one or more second filamentous fungal cells.

25 65. The substrate of claim 64, wherein the filamentous fungal ESTs are selected from the group consisting of *Acremonium*, *Aspergillus*, *Fusarium*, *Humicola*, *Mucor*, *Myceliophthora*, *Neurospora*, *Penicillium*, *Thielavia*, *Tolypocladium*, and *Trichoderma* ESTs.

30 66. The substrate of claim 65, wherein the filamentous fungal ESTs are *Fusarium* ESTs.

67. The substrate of claim 66, wherein the filamentous fungal ESTs are *Fusarium venenatum* ESTs.
- 5 68. The substrate of claim 67, wherein the *Fusarium venenatum* ESTs are selected from the group consisting of SEQ ID NOs. 1-3770, nucleic acid fragments of SEQ ID NOs. 1-3770, and nucleic acid sequences having at least 90% homology to SEQ ID NOs. 1-3770.
- 10 69. The substrate of claim 68, wherein the *Fusarium venenatum* ESTs are SEQ ID NOs. 1-3770.
70. The substrate of claim 68, wherein the *Fusarium venenatum* ESTs are nucleic acid sequences having at least 90% homology to SEQ ID NOs. 1-3770.
- 15 71. The substrate of claim 65, wherein the filamentous fungal ESTs are *Aspergillus* ESTs.
72. The substrate of claim 71, wherein the *Aspergillus* ESTs are *Aspergillus niger* ESTs.
- 20 73. The substrate of claim 72, wherein the *Aspergillus niger* ESTs are selected from the group consisting of SEQ ID NOs. 3771-4376, nucleic acid fragments of SEQ ID NOs. 3771-4376, and nucleic acid sequences having at least 90% homology to SEQ ID
- 25 NOs. 3771-4376.
74. The substrate of claim 73, wherein the *Aspergillus niger* ESTs are SEQ ID NOs. 3771-4376.
- 30 75. The substrate of claim 73, wherein the *Aspergillus niger* ESTs are nucleic acid sequences having at least 90% homology to SEQ ID NOs. 3771-4376.

76. The substrate of claim 71, wherein the *Aspergillus* ESTs are *Aspergillus oryzae* ESTs.

77. The substrate of claim 76, wherein the *Aspergillus oryzae* ESTs are selected from the group consisting of SEQ ID NOs. 4377-7401, nucleic acid fragments of SEQ ID NOs. 4377-7401, and nucleic acid sequences having at least 90% homology to SEQ ID NOs. 4377-7401.

78. The substrate of claim 77, wherein the *Aspergillus niger* ESTs are SEQ ID NOs. 4377-7401.

79. The substrate of claim 77, wherein the *Aspergillus oryzae* ESTs are nucleic acid sequences having at least 90% homology to SEQ ID NOs. 4377-7401.

80. The substrate of claim 65, wherein the filamentous fungal ESTs are *Trichoderma* ESTs.

81. The substrate of claim 80, wherein the filamentous fungal ESTs are *Trichoderma reesei* ESTs.

82. The substrate of claim 81, wherein the *Trichoderma reesei* ESTs are selected from the group consisting of SEQ ID NOs. 7402-7860, nucleic acid fragments of SEQ ID NOs. 7402-7860, and nucleic acid sequences having at least 90% homology to SEQ ID NOs. 7402-7860.

83. The substrate of claim 82, wherein the *Trichoderma reesei* ESTs are SEQ ID NOs. 7402-7860.

84. The substrate of claim 82, wherein the *Trichoderma reesei* ESTs are nucleic acid sequences having at least 90% homology to SEQ ID NOs. 7402-7860.

85. An isolated nucleic acid sequence comprising any of SEQ ID NOs. 1-7860.

Take on
page 325-
Seq ID 7404

86. The nucleic acid sequence of claim 85, wherein SEQ ID NOs. 1-3770 are obtained from *Fusarium venenatum*.

5 87. The nucleic acid sequence of claim 85, wherein SEQ ID NOs. 3771-4376 are obtained from *Aspergillus niger*.

88. The nucleic acid sequence of claim 85, wherein SEQ ID NOs. 4377-7401 are obtained from *Aspergillus oryzae*.

10

89. The nucleic acid sequence of claim 85, wherein SEQ ID NOs. 7402-7860 are obtained from *Trichoderma reesei*.